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    a)   Trp-R^1-X_7-R^1-R^1-R^2-X-Phe-Phe-Tyr-X-Thr-Glu-X_{8-9}-R$_1$-R^3-Arg-R^4-X_2-Trp

    b) X_3-Arg-X_2-Pro-Lys-X_3

    c)   X-Arg-X-Ile-X

    d) X_4-Phe-X_3-Asp-X_4-Tyr-Asp-X_2

    e)   Tyr-X_4-Gly-X_2-Gln-Gly-X_3-Ser-X_8

    f) X_6-Asp-Asp-X-Leu-X_3

wherein R^1 is Leu or Ile; R^2 is Gln or Arg; R^3 is Phe or Tyr; R^4 is Lys or His, and X_n represents the number n of consecutive unspecified amino acids;

and wherein the protein has telomerase catalytic activity when complexed with a telomerase RNA component.

120   (Amended)   The polynucleotide of claim 119, encoding a protein that comprises the structure Trp-Leu-X-Tyr-X_2-h-h-X-h-h-X-p-Phe-Phe-Tyr-X-Thr-Glu-X-p-X_3-p-X_3-Tyr-X-Arg-Lys-X_2-Trp; wherein h is a hydrophobic amino acid selected from Ala, Leu, Ile, Val, Pro, Phe, Trp, and Met; and p is a polar amino acid selected from Gly, Ser, Thr, Tyr, Cys, Asn and Gln.

121   (Amended)   The polynucleotide of claim 119, where structure a) further comprises Arg-Lys-X_2-Trp-X_2-Leu.
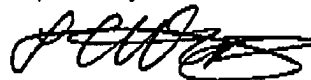
REMARKS

Claims 119-127 are pending in the application. With entry of this Supplemental Preliminary Amendment, claims 119-121 have been amended. The only change made herein is to use subscripts and superscripts to designate certain amino acid residues of the various motifs recited in the claims. Such use is helpful in distinguishing between coded amino acids and repeat residues, as defined in claim 119. No new matter has been introduced.

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        If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 650-326-2400 x 5209.

Respectfully submitted,

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Appendix: Marked-up version of claim amendments

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